Propositions

1. The integration of multiple biological data layers, for example genetic, transcriptomic, methylome and the microbiome data, leads to a more complete understanding of biological effects. (this thesis)

2. Both genetics and the environment influence the microbiome, DNA-methylation & gene-expression. (this thesis)

3. Commonly used medication can have negative influences on your "health". (this thesis)

4. Large-scale (perturbation) studies on the gut microbiome are needed to accurately identify relations between the host and the gut microbiome. (this thesis)

5. The gut microbiome is an attractive target for therapies aimed at improving lipid levels in blood. (this thesis)

6. Genetic risk factors affect both gene-expression and DNA-methylation, at a local and a distal level. (this thesis)

7. Genetic effects on expression and DNA-methylation are tissue-specific. (this thesis)

8. DNA-methylation changes reflect the altered abundance of transcription factors. (this thesis)

9. Analysis of individual genome-, methylome-, microbiome- and transcriptome profiles will become something to be performed on a daily basis for health monitoring.

10. In the coming years, integrative analysis of big data on DNA-methylation, the microbiome, gene expression and genetics will substantially change the healthcare system, all the way from your general practitioner to the ICU.

11. Open access science publications and open access to data and methods will greatly speed up the changes in healthcare and yield major benefits to the public and researchers.

12. A scientist works with others to discover the world around them; science is teamwork.